

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 22, 2003, 15:07:34 ; Search time 24 Seconds

(without alignments)
685.806 Million cell updates/sec

Title: US-09-745-506-37

Perfect score: 350
Sequence: 1 MDKALSLSLNDPASFASF.....LENKINILITSETRDPLQVY 350

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	350	100.0	350	1 NF3L_HUMAN	09gzt8 homo sapien
2	51	14.6	350	1 NF3L_MOUSE	09gzt8 mus musculu
3	10	2.9	366	1 YF59_STAM	09glt7 staphylococ
4	9	2.6	288	1 NIF3_YEAST	P53081 saccharomyc
5	7	2.0	119	1 RNPA_MYCPA	091719 mycobacteri
6	7	2.0	146	1 SSBS_XENLA	P09380 xenopus lae
7	7	2.0	148	1 SBR_XENLA	P09381 xenopus lae
8	7	2.0	150	1 COXA_HUMAN	P20674 homo sapien
9	7	2.0	221	1 IFB3_ARATH	09f559 arabidopsis
10	7	2.0	224	1 FLGA_YEREN	056892 yersinia en
11	7	2.0	224	1 MTOG_HUMAN	P15173 homo sapien
12	7	2.0	224	1 MTOG_MOUSE	P12579 mus musculu
13	7	2.0	224	1 MYOG_PIG	P49612 sus scrofa
14	7	2.0	249	1 Y382_NEIMA	091xg6 neisseria m
15	7	2.0	249	1 YK54_NEIMB	091xg9 neisseria m
16	7	2.0	250	1 YK54_PYRAB	09uvt3 pyrococcus
17	7	2.0	252	1 PYC4_ANASP	P29389 anabaena sp
18	7	2.0	278	1 Y3JC_SCHPO	094404 schizosach
19	7	2.0	287	1 MYOG_RAT	P20428 rattus norv
20	7	2.0	291	1 RS2_TREPA	083155 treponema p
21	7	2.0	292	1 A36A_DROME	09k557 drosophila
22	7	2.0	301	1 SYGA_SHEON	08e855 sheanella
23	7	2.0	312	1 RLMO_YEAST	P03117 saccharomyc
24	7	2.0	322	1 PGLB_HUMAN	099645 homo sapien
25	7	2.0	328	1 PLS1_MOUSE	091100 mus musculu
26	7	2.0	330	1 YH75_ARCFU	028499 archaeoglob
27	7	2.0	335	1 PLS1_RAT	P51825 rattus norv
28	7	2.0	348	1 RLMO_HAIMA	P15525 halocarcula
29	7	2.0	398	1 GPDI_YARLI	09uvt4 yarrowia li
30	7	2.0	431	1 ARAL_BACHD	09kca6 bacillus ha
31	7	2.0	445	1 EXTL_STAM	0991x0 staphylococ
32	7	2.0	477	1 MM03_HORSE	028397 equus cabal
33	7	2.0	502	1 YH60_MYCTU	006795 mycobacteri

34	7	2.0	507	1 YIK4_YEAST	P40486 saccharomyc
35	7	2.0	557	1 PAC1_PSES3	P15557 pseudomonas
36	7	2.0	577	1 PAC1_PSES3	005053 pseudomonas
37	7	2.0	577	1 UREL_MYCTU	P50042 mycobacteri
38	7	2.0	622	1 ABS_HUMAN	094v9 homo sapien
39	7	2.0	625	1 SYR_SULSO	097an1 sulfolobus
40	7	2.0	641	1 SAC2_YEAST	P39904 saccharomyc
41	7	2.0	709	1 ANDR_RABIT	P46699 oryctolagus
42	7	2.0	775	1 PLSB_MYCLE	09x7b0 mycobacteri
43	7	2.0	825	1 PHK_SCHPO	074770 schizosach
44	7	2.0	875	1 HIR2_YEAST	P32480 saccharomyc
45	7	2.0	884	1 ANDR_EULFC	097776 eulemur ful

ALIGNMENTS

RESULT 1	ID	NE3L_HUMAN	STANDARD:	PRT:	350 AA.
AC	09GZT8	09H2D2; 09HC18;			
DT	28-FEB-2003	(Rel. 41, Created)			
DT	28-FEB-2003	(Rel. 41, Last sequence update)			
DE	15-SEP-2003	(Rel. 42, Last annotation update)			
DE	NIF3-like protein 1 (Amyotrophic lateral sclerosis 2 chromosomal				
DE	region candidate gene protein 1) (M9018 protein) (MDS015).				
GN	NIF3L1 OR ALS2CR1.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A., AND SUBCELLULAR LOCATION.				
RX	MEDLINE=20573864; PubMed=11124544;				
RA	Tascou S., Uedelhoven J., Dixkens C., Nayerula K., Engel W.,				
RA	Burfeind P.;				
RT	*Isolation and characterization of a novel human gene, NIF3L1, and its				
RT	mouse ortholog, Nif3l1, highly conserved from bacteria to mammals.;				
RL	Cytogenet. Cell Genet. 90:330-336(2000).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=21100893; PubMed=11161814;				
RA	Hadano S., Yanagisawa Y., Skaug J., Fichter K., Nasir J.,				
RA	Martindale D., Koop B.F., Scherer S.W., Nicholson D.W., Rouleau G.A.,				
RA	Ikedo J.-E., Hayden M.R.;				
RT	*Cloning and characterization of three novel genes, ALS2CR1, ALS2CR2,				
RT	and ALS2CR3, in the juvenile amyotrophic lateral sclerosis (ALS2)				
RT	critical region at chromosome 2q33-q34: candidate genes for ALS2.;				
RN	Genomics 71:200-213(2001).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Brain;				
RL	Mao Y.M., Xie Y., Huang X.Y., Ying K., Dai J.L.;				
RL	Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RA	Huang C., Qian B., Yu Y., Gu W., Wang Y., Han Z., Chen Z.;				
RT	*Novel genes expressed in hematopoietic stem/progenitor cells from				
RT	myelodysplastic syndromes patient.;				
RL	Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Ovarian carcinoma;				
RA	Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,				
RA	Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,				
RA	Wagatsuna M., Hosofiri T., Faku Y., Kodaira H., Kondo H.,				
RA	Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,				
RA	Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,				
RA	Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K., Masuno Y.,				
RA	Ninomiyu K., Iwayanagi T.;				
RT	*NEO human cDNA sequencing project.;				
RL	Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.				
RN	[6]				

RP SEQUENCE FROM N.A.
 RC TISSUE-Skin;
 RA MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carinici P., Prange C.,
 RA Raha S.S., Loguanello N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE OPG0135 (NIF3) FAMILY.
 CC -----
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 CC -----
 DR EMBL: AF283538; AAC44846.1; ALT_INIT.
 DR EMBL: AB038949; BAB32499.1; -
 DR EMBL: AF060513; AAC43131.1; -
 DR EMBL: AF182416; AAC44952.1; -
 DR EMBL: AK023378; BAB14551.1; -
 DR EMBL: BC007654; AAH07654.1; ALT_INIT.
 DR Genew: HGNC:13390; NIF3L.
 DR InterPro: IPR002678; DUF34.
 DR Pfam: PF01784; NIF3; 1.
 DR TIGRFAMS: TIGR00486; TIGR00486.1.
 DR CONFLICT 77 82 TWNTWK -> NLEHMR (IN REF. 4).
 FT SEQUENCE 350 AA; 38983 MW; 81F1A5AD3B25ED7 CRC64;
 SQ
 Query Match 100.0%; Score 350; DB 1; Length 350;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 301 ASOGINVLCEHSHNTERGFLSDRLMDLSHLENKINILITSETDRDPLQV 350
 RESULT 2
 ID NIF3L_MOUSE STANDARD; PRT; 350 AA.
 AC OPG080; Q8D098;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE NIF3-like protein 1.
 CN NIF3L.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RX MEDLINE=20573864; PubMed=11124544;
 RA Tascou S., Uedelhoven J., Dixkens C., Nayeria K., Engel W.,
 RA Burfelnd P.;
 RT "Isolation and characterization of a novel human gene, NIF3L, and its
 RT mouse ortholog, Nif3l, highly conserved from bacteria to mammals.";
 RL Cytogenet. Cell Genet. 90:330-336(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Atawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
 RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant H.,
 RA Felschmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nakado I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli P., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bolt C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilmink L.,
 RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kotsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).
 CC -1- TISSUE SPECIFICITY: Ubiquitous.
 CC -----
 CC -1- SIMILARITY: BELONGS TO THE OPG0135 (NIF3) FAMILY.
 CC -----
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 CC -----
 DR EMBL: AF284439; AAC45961.1; ALT_INIT.
 DR EMBL: AK011670; BAB27769.1; ALT_INIT.
 DR InterPro: IPR002678; DUF34.
 DR MGD: MGI:1929485; NIF3L.
 DR TIGRFAMS: TIGR00486; TIGR00486.1.
 DR CONFLICT 164 164 G -> S (IN REF. 2).
 FT CONFLICT 178 178 E -> K (IN REF. 2).
 FT CONFLICT 191 191 L -> F (IN REF. 2).
 FT CONFLICT 195 195 L -> Q (IN REF. 2).
 FT CONFLICT 198 198 L -> F (IN REF. 2).
 FT CONFLICT 208 208 T -> I (IN REF. 2).
 FT SEQUENCE 350 AA; 38828 MW; B0FA71503CF086 CRC64;

Query Match 14.6%; Score 51; DB 1; Length 350;
 Best Local Similarity 100.0%; Pred. No. 1.8e-43;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKALLSLNDFASLSFAESMDNVGLLEPPSPHVTNLTFLNDLTEEVN 51
 DB 1 MDKALLSLNDFASLSFAESMDNVGLLEPPSPHVTNLTFLNDLTEEVN 51

RESULT 3
 YF59_STRAAM STANDARD; PRT; 366 AA.

ID YF59_STRAAM STANDARD; PRT; 366 AA.
 AC 099TT7;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE Hypothetical protein SAV1559/SA1388.
 GN SAV1559 OR SA1388.
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699), and
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158678, 158679;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Mu50 / ATCC 700699, and N315;
 RX MEDLINE=21311952; PubMed=11418146;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
 Kanamori M., Matsunari H., Maruyama A., Murakami H., Hosoyma A.,
 Mizutani-U I., Takahashi N.K., Sawano T., Inoue R.-I., Kato C.,
 Sekimizu K., Hirakawa H., Kubara S., Goto S., Yabuzaki J.,
 Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus."
 RL Lancet 357:1225-1240(2001).
 CC -1- SIMILARITY: BELONGS TO THE UPF0135 (NIF3) FAMILY.
 CC -----
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 CC -----
 CC EMBL: AP003362; BAB57721.1; -;
 DR EMBL: AP003362; BAB57721.1; -;
 DR EMBL: AP003362; BAB57721.1; -;
 DR PIR: F89936; F89936.
 DR InterPro: IPR002678; DUF34.
 DR Pfam: PF01784; NIF3; 1.
 DR TIGRPFAMs: TIGR00486; TIGR00486; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 366 AA; 41075 MW; CA7D5FADF78FFFA CRC64;

Query Match 2.9%; Score 10; DB 1; Length 366;
 Best Local Similarity 100.0%; Pred. No. 0.047;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 AESMDNVGLL 28
 DB 19 AESMDNVGLL 28

RESULT 4
 NIF3_YEAST STANDARD; PRT; 288 AA.
 ID NIF3_YEAST STANDARD; PRT; 288 AA.
 AC P53081;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE NG1-interacting factor 3.

GN NIF3 OR YGL221C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288C;
 RX MEDLINE=97435481; PubMed=9290212;
 RA Rieger M., Brueckner M., Schaefer M., Mueller-Auer S.,
 RT "Sequence analysis of 203 kilobases from Saccharomyces cerevisiae
 chromosome VII."
 RL Yeast 13:1077-1090(1997).
 CC -1- SIMILARITY: BELONGS TO THE UPF0135 (NIF3) FAMILY.
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 CC -----
 CC EMBL: Z72743; CAA96937.1; -;
 DR PIR: S64243; S64243.
 DR SGD: S0003189; NIF3.
 DR InterPro: IPR002678; DUF34.
 DR Pfam: PF01784; NIF3; 1.
 DR TIGRPFAMs: TIGR00486; TIGR00486; 1.
 SQ SEQUENCE 288 AA; 31888 MW; B6AB6E48AFA776A CRC64;

Query Match 2.6%; Score 9; DB 1; Length 288;
 Best Local Similarity 100.0%; Pred. No. 0.38;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 312 HSNTERGFL 320
 DB 252 HSNTERGFL 260

RESULT 5
 RNPA_MYCPA STANDARD; PRT; 119 AA.
 ID RNPA_MYCPA STANDARD; PRT; 119 AA.
 AC 09L7L9;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ribonuclease P protein component (EC 3.1.26.5) (RNaseP protein) (RNase
 P protein) (Protein C5).
 GN RNPA.
 OS Mycobacterium paratuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1770;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang Q., Kapur V.;
 RT "Genomic organization of the Mycobacterium avium subsp.
 RT paratuberculosis origin of replication region."
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: RNaseP catalyzes the removal of the 5'-leader sequence
 CC from pre-tRNA to produce the mature 5' terminus. It can also
 CC cleave other RNA substrates such as 4.5S RNA. The protein
 CC component plays an auxiliary but essential role in vivo by binding
 CC to the 5'-leader sequence and broadening the substrate specificity
 CC of the ribozyme (by similarity).
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of RNA, removing 5'-
 CC extra-nucleotide from tRNA precursor.
 CC -1- SUBUNIT: Consists of a catalytic RNA component (M1 or rnpB) and a
 CC protein subunit (by similarity).
 CC -1- SIMILARITY: BELONGS TO THE RNPA FAMILY.
 CC -----
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CC -----
 CC EMBL; AF222789; AAF33695.1; -
 CC HSSP; P25814; 1A6F.
 CC HAMAP; MF_00227; -; 1.
 CC InterPro; IPR000100; Ribonuclease_P.
 CC Pfam; PF00823; Ribonuclease_P; 1.
 CC ProDom; PD003629; Ribonuclease_P; 1.
 CC TIGRFAMs; TIGR00188; rnpA; 1.
 CC PROSITE; PS00648; RIBONUCLEASE_P; 1.
 CC KJ Hydroxylase; Nuclease; Endonuclease; tRNA processing; RNA-binding.
 CC SEQUENCE 119 AA; 13131 MW; BBB6C38A11764721 CRC64;

Query Match 2.0%; Score 7; DB 1; Length 119;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 84 RLVTAL 90
 |||||
 DB 85 RLVTAL 91

RESULT 6
 SSB_XENLA STANDARD; PRT; 146 AA.
 ID SSB_XENLA STANDARD; PRT; 146 AA.
 AC P09380;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Single-stranded DNA-binding protein S, mitochondrial precursor (Mt-
 DE SSB-S) (Mt-SSB 1).
 GN MTSSB.
 OS Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 CC Xenopodinae; Xenopus.
 CC NCBI_TaxID=8355;
 RN RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RX MEDLINE=91334145; PubMed=1870981;
 RA Tifant V., Barat-Gueride M., Biji J., Didonato S., Zeviani M.;
 RT "A full-length cDNA encoding a mitochondrial DNA-specific single-
 RT stranded DNA binding protein from Xenopus laevis.";
 RL Nucleic Acids Res. 19:4291-4291(1991).
 RN RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal muscle;
 RX MEDLINE=97169147; PubMed=9016954;
 RA Champagne A.M., Dufresne C., Viney L., Gueride M.;
 RT "Cloning, sequencing and expression of the two genes encoding the
 RT mitochondrial single-stranded DNA-binding protein in Xenopus
 RT laevis.";
 RL Gene 184:65-71(1997).
 RN RP SEQUENCE OF 18-142.
 RX MEDLINE=92061073; PubMed=1952953;
 RA Ghir R., Lecler J.-P., Dufresne C., Barat-Gueride M.;
 RT "Primary structure of the two variants of Xenopus laevis mtSSB, a
 RT mitochondrial DNA binding protein.";
 RL Arch. Biochem. Biophys. 291:395-400(1991).
 RN RP SEQUENCE OF 18-41.
 RX MEDLINE=88296837; PubMed=3042458;
 RA Mahoungou C., Ghir R., Lecler J.-P., Mynotte B., Barat-Gueride M.;
 RT "The amino-terminal sequence of the Xenopus laevis mitochondrial SSB
 RT is homologous to that of the Escherichia coli protein.";
 RL FEBS Lett. 235:267-270(1988).

CC -1- FUNCTION: This protein binds preferentially and cooperatively to
 CC ss-DNA, and can under certain conditions stimulate the activity of
 CC DNA polymerase. Probably involved in mitochondrial DNA
 CC replication.
 CC -1- SUBUNIT: Homotrimer (Probable).
 CC -1- SUBCELLULAR LOCATION: Mitochondrial.
 CC -1- SIMILARITY: BELONGS TO THE SSB FAMILY.

CC -----
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CC -----
 CC EMBL; X59285; CAA41976.1; -
 CC EMBL; X83673; CAA58647.1; -
 CC PIR; JC6173; JC6173.
 CC HSSP; Q04837; 30DL.
 CC InterPro; IPR000424; SSB_protein.
 CC Pfam; PF00436; SSB; 1.
 CC TIGRFAMs; TIGR00621; ssb; 1.
 CC PROSITE; PS00735; SSB_1; 1.
 CC PROSITE; PS00736; SSB_2; 1.
 CC KW DNA-binding; DNA replication; Mitochondrion; Transit peptide.
 CC TRANSIT 17
 CC CHAIN 18 146
 CC SEQUENCE 146 AA; 16743 MW; F97D77149A25B3E CRC64;

Query Match 2.0%; Score 7; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 319 FLSDLD 325
 |||||
 DB 138 FLSDLD 144

RESULT 7
 SSB_XENLA STANDARD; PRT; 148 AA.
 ID SSB_XENLA STANDARD; PRT; 148 AA.
 AC P09381; 013264;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Single-stranded DNA-binding protein R, mitochondrial precursor (Mt-
 DE SSB-R) (Mt-SSB 2).
 GN MTSSB2.
 OS Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 CC Xenopodinae; Xenopus.
 CC NCBI_TaxID=8355;
 RN RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal muscle;
 RX MEDLINE=97169147; PubMed=9016954;
 RA Champagne A.M., Dufresne C., Viney L., Gueride M.;
 RT "Cloning, sequencing and expression of the two genes encoding the
 RT mitochondrial single-stranded DNA-binding protein in Xenopus
 RT laevis.";
 RL Gene 184:65-71(1997).
 RN RP SEQUENCE OF 18-99.
 RX MEDLINE=92061073; PubMed=1952953;
 RA Ghir R., Lecler J.-P., Dufresne C., Barat-Gueride M.;
 RT "Primary structure of the two variants of Xenopus laevis mtSSB, a
 RT mitochondrial DNA binding protein.";
 RL Arch. Biochem. Biophys. 291:395-400(1991).
 RN RP PRELIMINARY SEQUENCE OF 18-38.
 RX MEDLINE=88296837; PubMed=3042458;

RA Mahoungou C., Ghir R., Lecaer J.-P., Mignotte B., Barot-Gueride M.;
 RT "The amino-terminal sequence of the Xenopus laevis mitochondrial SSB
 is homologous to that of the Escherichia coli protein.";
 RL FEBS Lett. 235:267-270(1988).
 CC
 CC -1- FUNCTION: This protein binds preferentially and cooperatively to
 ss-DNA, and can under certain conditions stimulate the activity of
 CC DNA polymerase. Probably involved in mitochondrial DNA
 CC replication.
 CC
 CC -1- SUBUNIT: Homotrimer (Probable).
 CC
 CC -1- SUBCELLULAR LOCATION: Mitochondrial.
 CC
 CC -1- SIMILARITY: BELONGS TO THE SSB FAMILY.
 CC
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 CC
 CC -----
 DR EMBL: J83674; CAA58648.1; -
 DR PIR: JC6172; JC6172.
 DR HSSP: Q04837; S0UL.
 DR InterPro: IPR000424; SSB_protein.
 DR Pfam: PF00436; SSB; 1.
 DR TIGRfam: TIGR00621; ssb; 1.
 DR PROSITE: PS00735; SSB_1; 1.
 DR PROSITE: PS00736; SSB_2; 1.
 DR DNA-binding; DNA replication; Mitochondrion; Transit peptide.
 FT TRANSIT 1 17
 FT CHAIN 18 148
 FT CONFLICT 49 49 D -> E (IN REF. 2).
 SO SEQUENCE 148 AA; 16929 MW; 6DDA54C91779E803 CRC64;
 QY Query Match 2.0%; Score 7; DB 1; Length 148;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 319 FLSDLRD 325
 140 FLSDLRD 146
 DB
 RESULT 8
 ID COXA_HUMAN STANDARD; PRT; 150 AA.
 AC P20674; P30045;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cytochrome c oxidase polypeptide Va, mitochondrial precursor
 DE (EC 1.9.3.1).
 GN COX5A.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=89172069; PubMed=2853101;
 RA Rizzuto R., Nakase H., Zeviani M., Dimauro S., Schon E.A.;
 RT "Subunit Va of human and bovine cytochrome c oxidase is highly
 RT conserved.";
 RL Gene 69:245-256(1988).
 RN [2]
 RP SEQUENCE OF 42-52.
 RC TISSUE=Liver;
 RX MEDLINE=9417969; PubMed=8313870;
 RA Hughes G.J., Fritiger S., Paquet N., Pasquall C., Sanchez J.-C.,
 RA Tisot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.;
 RT "Human liver protein map: update 1993.";
 RL Electrophoresis 14:1216-1222(1993).
 RN [3]

RP SEQUENCE OF 56-64 AND 73-80.
 RC TISSUE=Heart;
 RX MEDLINE=9607936; PubMed=7498159;
 RA Kovalyov L.I., Shishkin S.S., Efimochkin A.S., Kovalyova M.A.,
 RA Eshova E.S., Egorov T.A., Musalyanov A.K.;
 RT "The major protein expression profile and two-dimensional protein
 RT database of human heart.";
 RL Electrophoresis 16:1160-1169(1995).
 CC
 CC -1- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME C
 CC OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.
 CC
 CC -1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferrocyclochrome
 CC c + 2 H(2)O.
 CC
 CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
 CC
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VA FAMILY.
 CC
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 CC
 CC -----
 DR EMBL: M22760; AAA99220.1; -
 DR PIR: JT0342; OTHU5A.
 DR SWISS-2DPAGE: P20674; HUMAN.
 DR HSC-2DPAGE: P20674; HUMAN.
 DR Slens-2DPAGE: P20674; -
 DR Genew: HGNC:2267; COX5A.
 DR MIM: 603773; -
 DR GO: GO:0004129; F:cytochrome c oxidase activity; TAS.
 DR GO: GO:0005489; F:electron transporter activity; TAS.
 DR InterPro: IPR003204; Cyt_C-ox5A.
 DR Pfam: PF02284; COX5A; 1.
 DR Oxidoreductase; Heme; Mitochondrion; Inner membrane; Transit peptide.
 FT TRANSIT 1 41
 FT CHAIN 42 150
 FT CHAIN 1 150 CYTOCHROME C OXIDASE POLYPEPTIDE VA.
 SO SEQUENCE 150 AA; 16774 MW; 84CDAF468BC9C85 CRC64;
 QY Query Match 2.0%; Score 7; DB 1; Length 150;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 10 LNDPAST 16
 99 LNDPAST 105
 DB
 RESULT 9
 ID IFP3_ARATH STANDARD; PRT; 221 AA.
 AC G9PKS9; O64928;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Eukaryotic translation initiation factor 4E type 3 (eIF-4E type 3)
 DE (eIF4E type 3) (mRNA cap-binding protein type 3) (Novel cap-binding
 DE protein) (ncBP).
 GN AT5G16110 OR MKG7.7.
 GN Arabidopsis thaliana (Mouse-ear cress).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=98221164; PubMed=9553087;
 RA Rud R.A., Kuhlman C., Goss D.J., Browning K.S.;
 RT "Identification and characterization of a novel cap-binding protein
 RT from Arabidopsis thaliana.";
 RL J. Biol. Chem. 273:10325-10330(1998).
 RN [2]
 RP SEQUENCE FROM N.A.

RC STRAIN-cv. Columbia;
 RX MEDLINE-9840384; Pubmed-9734815;
 RA Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. VI.
 RT Sequence features of the regions of 1,367,185 bp covered by 19
 RT physically assigned pl and TAC clones."
 RL DNA Res. 5:203-216(1998).
 RN [3].
 RP SEQUENCE FROM N.A.
 RC STRAIN-cv. Columbia;
 RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
 RT "Riken Arabidopsis full length cDNA clones (RAFLs) sequenced by the
 RT SSP consortium (Salk/Stanford/PGSC)."
 RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Recognizes and binds the 7-methylguanosine-containing
 CC mRNA "cap" during an early step in the initiation of protein
 CC synthesis and facilitates ribosome binding by inducing the
 CC unwinding of the mRNAs secondary structures.
 CC -1- SUBUNIT: EIF4E is a trimer composed of EIF4E, EIF4G and EIF4A
 CC (which can cycle in and out of the complex) (by similarity).
 CC -1- SIMILARITY: BELONGS TO THE EUKARYOTIC INITIATION FACTOR 4E FAMILY.
 CC -----
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 CC -----
 DR EMBL: AF028809; AAC17220.1; -
 DR EMBL: AB012246; BAB09469.1; -
 DR EMBL: AY092964; AAM12963.1; -
 DR EMBL: AY093208; AAM13207.1; -
 DR EMBL: AY114562; AAM47881.1; -
 DR InterPro: IPR001040; TIF-EIF4E.
 DR Pfam: PF01652; IF4E; 1.
 DR ProDom: PD003697; TIF-EIF4E; 1.
 DR PROSITE: PS00813; IF4E; FALSE-NEG.
 KW Initiation factor; Protein biosynthesis; RNA-binding;
 KW Multigene family.
 FT CONFIDENT 42 D -> L (IN REF. 1).
 SQ SEQUENCE 221 AA; 25745 MW; FE484870E9769C6F CRC64;
 Query Match 2.0%; Score 7; DB 1; Length 221;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 242 IKRHKL 248
 DB 187 IKRHKL 193
 RESULT 10
 FLGA_YEREN
 ID FLGA_YEREN STANDARD: PRT; 224 AA.
 AC Q56892;
 DT 01-NOV-1997 (Rel. 35; Created)
 DT 01-NOV-1997 (Rel. 35; Last sequence update)
 DT 28-FEB-2003 (Rel. 41; Last annotation update)
 DE Flagella basal body P-ring formation protein flga precursor.
 GN FLGA.
 OS Yersinia enterocolitica.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 OX NCBI_Taxid=630;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-W1024 / Serotype O:9;
 RA Fauconnet A., Allaoui A., van Elsen A., Cornelis G., Bollen A.;
 RL Submitted (May-1995) to the EMBL/GenBank/DDAI databases.
 CC -1- FUNCTION: INVOLVED IN THE ASSEMBLY PROCESS OF THE P-RING

CC FORMATION. IT MAY ASSOCIATE WITH FLGE ON THE ROD CONSTITUTING A
 CC STRUCTURE ESSENTIAL FOR THE P-RING ASSEMBLY OR MAY ACT AS A
 CC MODULATOR PROTEIN FOR THE P-RING ASSEMBLY (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Periplasmic (probable).
 CC -1- SIMILARITY: BELONGS TO THE FLGA FAMILY.
 CC -----
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 CC -----
 DR EMBL: 248169; CAA88191.1; -
 DR PIR: S54218; S54218.
 DR InterPro: IPR004924; FLGA.
 DR Pfam: PF03240; FLGA; 1.
 KW Flagella; Periplasmic; Signal.
 FT SIGNAL 1 26 POTENTIAL.
 FT CHAIN 27 224 FLAGELLA BASAL BODY P-RING FORMATION
 FT PROTEIN FLGA.
 SQ SEQUENCE 224 AA; 24351 MW; B98B74FBC7862A49 CRC64;
 Query Match 2.0%; Score 7; DB 1; Length 224;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 262 ESQVKV 268
 DB 45 ESQVKV 51
 RESULT 11
 MYOG_HUMAN
 ID MYOG_HUMAN STANDARD: PRT; 224 AA.
 AC P15173;
 DT 01-APR-1990 (Rel. 14; Created)
 DT 01-DEC-1992 (Rel. 24; Last sequence update)
 DT 15-SEP-2003 (Rel. 42; Last annotation update)
 DE Myogenin (Myogenic factor Myf-4).
 GN MYOG OR MYF4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-92064650; Pubmed-1659574;
 RA Salminen A., Braun T., Buchberger A., Juers S., Winter B.,
 RA Arnold H.H.;
 RT "Transcription of the muscle regulatory gene Myf4 is regulated by
 RT serum components, peptide growth factors and signaling pathways
 RT involving G proteins."
 RL J. Cell Biol. 115:905-917(1991).
 RN [2]
 RP PRELIMINARY SEQUENCE FROM N.A.
 RC TISSUE-Skeletal muscle;
 RX MEDLINE-90059960; Pubmed-2583111;
 RA Braun T., Bober E., Buschhausen-Denker G., Kohltz S., Grzeschik K.-H.,
 RA Arnold H.H.;
 RT "Differential expression of myogenic determination genes in muscle
 RT cells: possible autoactivation by the Myf gene products."
 RL EMBO J. 8:3617-3625(1989).
 RN [3]
 RP REVISIONS.
 RA Braun T., Bober E., Buschhausen-Denker G., Kohltz S., Grzeschik K.-H.,
 RA Arnold H.H.;
 RL EMBO J. 9:592-592(1990).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Muscle;
 RX MEDLINE-22388257; Pubmed-12477932;

RA Strausberg R.L., Felding A.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stopleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mollaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Helyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scheraga A., Schein J.E., Jones S.J.M., Maria W.A.,
RT Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: INVOLVED IN MUSCLE DIFFERENTIATION (MYOGENIC FACTOR).
CC INDICES FIBROBLASTS TO DIFFERENTIATE INTO MYOBLASTS. PROBABLE
CC SEQUENCE SPECIFIC DNA-BINDING PROTEIN.
CC -1- SUBUNIT: Efficient DNA binding requires dimerization with another
CC BHLH protein.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
CC TRANSCRIPTION FACTORS. "MYOGENIC FACTORS" SUBFAMILY.
CC -----
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CC -----
DR EMBL: X61155; CAA44080.1; -;
DR EMBL: X17651; CAA35641.1; ALT_SEQ.
DR EMBL: BC006347; AA06347.1; -;
DR PIR: A41128; A41128.
DR HSSP: P10085; IMDY.
DR TRNSPAC: T00520; -;
DR Genew: HGNC:7612; MYOG.
DR MIM: 159980; -;
DR GO: GO:0003700; F:transcription factor activity; TAS.
DR GO: GO:0007519; P:myogenesis; TAS.
DR InterPro: IPR001092; BHLH_basic.
DR InterPro: IPR002546; Basic.
DR Pfam: PF01586; Basic; 1.
DR Pfam: PF00010; HLF; 1.
DR SMART: SM00520; BASIC; 1.
DR SMART: SM00353; HLF; 1.
DR PROSITE: PS00038; HLF_1; 1.
DR PROSITE: PS00888; HLF_2; 1.
DR Myogenesis; Differentiation; Developmental protein; Nuclear protein;
KW DNA-binding.
KW DNA_BIND 81 93 BASIC DOMAIN
FT DOMAIN 94 133 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
SQ SEQUENCE 224 AA; 25037 MW; 91421D69B5751FB CRC64;
Query Match 2.0%; Score 7; DB 1; Length 224;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AC P12979;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE MyoG.
DE MyoG (MYO1-related protein).
GN MYOG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RP STRAIN-BALB/C; TISSUE=Muscle;
RX MEDLINE=89306601; PubMed=2473006;
RA Edmondson D.G., Olson E.N.;
RT "A gene with homology to the myc similarity region of MyoD is
RT expressed during myogenesis and is sufficient to activate the muscle
RT differentiation program.";
RL Genes Dev. 3:628-640(1989).
RN [2]
RP ERRATUM.
RX MEDLINE=91032996; PubMed=2172083;
RA Edmondson D.G., Olson E.N.;
RL Genes Dev. 4:1450-1450(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=92375033; PubMed=1324403;
RA Edmondson D.G., Cheng T.C., Cserjesi P., Chakraborty T., Olson E.N.;
RT "Analysis of the myogenin promoter reveals an indirect pathway for
RT positive autoregulation mediated by the muscle-specific enhancer
RT factor MEF-2.";
RL Mol. Cell. Biol. 12:3665-3677(1992).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=90368705; PubMed=2168405;
RA Fujisawa-Senara A., Nabeshima Y., Hosoda Y., Oblinata T., Nabeshima Y.;
RT "Myogenin contains two domains conserved among myogenic factors.";
RL J. Biol. Chem. 265:15219-15223(1990).
CC -1- FUNCTION: INVOLVED IN MUSCLE DIFFERENTIATION (MYOGENIC FACTOR).
CC INDICES FIBROBLASTS TO DIFFERENTIATE INTO MYOBLASTS. PROBABLE
CC SEQUENCE SPECIFIC DNA-BINDING PROTEIN.
CC -1- SUBUNIT: Efficient DNA binding requires dimerization with another
CC BHLH protein.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
CC TRANSCRIPTION FACTORS. "MYOGENIC FACTORS" SUBFAMILY.
CC -----
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CC -----
DR EMBL: M95800; AAB59676.1; -;
DR EMBL: X15784; CAA33785.1; ALT_SEQ.
DR EMBL: D90156; BAA1487.1; -;
DR PIR: A35882; A36675.
DR HSSP: P10085; IMDY.
DR TRNSPAC: T00528; -;
DR MGD: MGI:97276; Myog.
DR InterPro: IPR002546; Basic.
DR InterPro: IPR001092; HLF_Basic.
DR Pfam: PF01586; Basic; 1.
DR Pfam: PF00010; HLF; 1.
DR SMART: SM00520; BASIC; 1.
DR SMART: SM00353; HLF; 1.
DR PROSITE: PS00038; HLF_1; 1.
DR PROSITE: PS00888; HLF_2; 1.
DR Myogenesis; Differentiation; Developmental protein; Nuclear protein;
KW DNA-binding.
FT DNA_BIND 81 93 BASIC DOMAIN.

FT DOMAIN 94 133 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
 SQ SEQUENCE 224 AA; 25203 MW; CC7352C1EDF9D3D8 CRC64;
 Query Match 2.0%; Score 7; DB 1; Length 224;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ALLSLN 11
 Db 134 ALLSLN 140

RESULT 13
 ID MYOG_PIG STANDARD; PRT; 224 AA.
 AC P49812;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Myogenin.
 GN MYOG.
 OS Sus scrofa (Pig).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 CX NCBI_TaxID=9623;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RA Briley G.P., Reedy J.M., Grant A.L., Bidwell C.A.;
 RL submitted (SEP-1994) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Soumillion A., Erkens J.H.F., Lenstra J.A., Zilstra C.,
 RA Bosma A.A., Te Pas M.F.W.;
 RL submitted (DEC-1995) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: INVOLVED IN MUSCLE DIFFERENTIATION (MYOGENIC FACTOR).
 CC INDUCES FIBROBLASTS TO DIFFERENTIATE INTO MYOBLASTS. PROBABLE
 CC SEQUENCE SPECIFIC DNA-BINDING PROTEIN.
 CC -1- SUBUNIT: Efficient DNA binding requires dimerization with another
 CC BHLH protein.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
 CC TRANSCRIPTION FACTORS. "MYOGENIC FACTORS" SUBFAMILY.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL; U14331; AB97306.1; -;
 DR EMBL; X89007; CAA61410.1; -;
 DR HSSP; P10085; IMDY.
 DR InterPro: IPR002546; Basic.
 DR InterPro: IPR001092; HLH_basic.
 DR Pfam; PF01586; Basic; 1.
 DR Pfam; PF00010; HLH; 1.
 DR SMART; SMO0520; BASIC; 1.
 DR SMART; SMO0353; HLH; 1.
 DR PROSITE; PS00038; HLH_1; 1.
 DR PROSITE; PS50888; HLH_2; 1.
 KM Myogenesis; Differentiation; Developmental protein; Nuclear protein;
 KW DNA-binding.
 FT DNA_BIND 81 93 BASIC DOMAIN.
 FT DOMAIN 94 133 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
 SQ SEQUENCE 224 AA; 25085 MW; 29A12219ACBF2B5 CRC64;

Query Match 2.0%; Score 7; DB 1; Length 224;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ALLSLN 11
 Db 134 ALLSLN 140

RESULT 14
 ID Y382_NEIMA STANDARD; PRT; 249 AA.
 AC O9JWG6;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein NMA0382.
 GN NMA0382.
 OS Neisseria meningitidis (serogroup A).
 CC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 CC Neisseriaceae; Neisseria.
 CX NCBI_TaxID=65699;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Z2491 / Serogroup A / Serotype 4a;
 RX MEDLINE=20222556; PubMed=10761919;
 RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
 RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
 RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
 RA Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
 RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
 RA Whitehead S., Spratt B.G., Barrall B.G.;
 RT "Complete DNA sequence of a serogroup A strain of Neisseria
 RT meningitidis Z2491.";
 RL Nature 404:502-506(2000).
 CC -1- SIMILARITY: BELONGS TO THE UPF0135 (NIF3) FAMILY.
 CC -----
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 CC -----
 CC EMBL; AL162753; CAB83683.1; -;
 DR PIR; D81954; D81954.
 DR InterPro: IPR002678; DUF34.
 DR Pfam; PF01784; NIF3; 1.
 DR TIGRfams; TIGR00486; TIGR00486; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 249 AA; 27484 MW; FDE2FE12B3FC216F CRC64;

Query Match 2.0%; Score 7; DB 1; Length 249;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 285 DLYTGE 291
 Db 190 DLYTGE 196

RESULT 15
 ID YK34_NEIMB STANDARD; PRT; 249 AA.
 AC O9JWG9;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein NMB2054.
 GN NMB2054.
 OS Neisseria meningitidis (serogroup B).
 CC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 CC Neisseriaceae; Neisseria.
 CX NCBI_TaxID=491;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-MC58 / Serogroup B;
 RX MEDLINE-20175755; PubMed-10710307;
 RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
 RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
 RA Nelson W.C., Gwinn M.L., Deboy R., Peterson J.D., Hickey E.K.,
 RA Hart D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
 RA Mason T., Ciecko A., Parksey D.S., Blair E., Ciltone H., Clark E.B.,
 RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
 RA Gall J., Scarlato V., Maignani V., Plizza M., Grandi G., Sun L.,
 RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.,
 RT *Complete genome sequence of Neisseria meningitidis serogroup B strain
 MC58.";
 RL Science 287:1809-1815(2000).
 CC -1- SIMILARITY: BELONGS TO THE UPF0135 (NIF3) FAMILY.
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 CC -----
 CC EMBL: AE002555; AAF42374.1; -
 DR PIR: G81011; G81011.
 DR TIGR: NMB2054; -
 DR InterPro: IPR002678; DUF34.
 DR Pfam: PF01784; NIF3; 1
 DR TIGRFAMs: TIGR00486; TIGR00486; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 249 AA; 27417 MW; 58EC0E47B6AE27B2 CRC64;

Query Match 2.0%; Score 7; DB 1; Length 249;
 Best local Similarity 100.0%; Pred No. 35;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 285 DLYLTGE 291
 |||||
 Db 190 DLYLTGE 196

Search completed: August 22, 2003, 15:17:31
 Job time : 25 secs

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